**Figure 1**

```
    1                                                            50
1   MSDRQAALDM ALKQIEKQFG KGSIMKLGEQ UEURISUVPS GSLALDAALG
2   MSDRQAALDM ALKQIEKQFG KGSIMKLGEK TDTRISTVPS GSLALDTALG
3   MSDRQAALDM ALKQIEKQFG KGSIMKLGEK TDTRISTVPS GSLALDTALG
4   MSDRQAALDM ALKQIEKQFG KGSIMKLGEK TDTRISTVPS GSLALDTALG

    51                                                          100
1   VGGYPRGRII EVYGPESSGK UUVALHAIAE VQQQGGQAAF IDADUALDPV
2   IGGYPRGRII EVYGPESSGK TTVALHAIAE VQEKGGQAAF IDAEHALDPV
3   IGGYPRGRII EVYGPESSGK TTVALHAIAE VQQQR.TSAF IDAEHALDPV
4   IGGYPRGRII EVYGPESSGK TTVALHAIAE VQQQR.TSAF IDAEHALDPV

    101                                                         150
1   YAQKLGVNID ELLLSQPDUG EQALEIAEAL VRSGAVDIVV IDSVAALVPK
2   YAQKLGVNIE ELLLSQPDTG EQALEIAEAL VRSGAVDIVV VDSVAALVPK
3   YAQKLGVNIE ELLLSQPDTG EQALEIAEAL VRSGAVDIVV VDSVAALVPK
4   YAQKLGVNIE ELLLSQPDTG EQALEIAEAL VRSGAVDIVV VDSVAALVPK

    151                                                         200
1   AEIEGDMGDS HVGLQARLMS QALRKLSGAI NKSKUIAIFI NQIREKVGVM
2   AEIEGDMGDS HVGLQARLMS QALRKLSGAI NKSKTIAIFI NQIREKVGVM
3   AEIEGDMGDS HVGLQARLMS QALRKLSGAI NKSKTIAIFI NQIREKVGVM
4   AEIEGDMGDS HVGLQARLMS QALRKLSGAI NKSKTIAIFI NQIREKVGVM

    201                                                         250
1   FGNPEUUPGG RALKFYSSVR LEVRRAEQLK QGNDVMGNKU KIKVVKNKVA
2   FGNPETTPGG RALKFYSSVR LEVRRAEQLK QGNDVMGNKT RIKVVKNKVA
3   FGNPETTPGG RALKFYSSVR LEVRRAEQLK QGNDVMGNKT KIKVVKNKVA
4   FGNPETTPGG RALKFYSSVR LEVRRAEQLK QGNDVMGNKT KIKVVKNKVA

    251                                                         300
1   PPFRUAEVDI MYGEGISKEG EIIDLGUELD IVQKSGAWYS YQEERLGQGR
2   PPFRTAEVDI MYGEGISKEG EIIDLGTELD IVQKSGSWYS YEEERLGQGR
3   PPFRTAEVDI MYGEGISKEG EIIDLGTELD IVQKSGSWYS YEEERLGQGR
4   PPFRTAEVDI MYGEGISKEG EIIDLGTELD IVQKSGSWYS YEEERLGQGR

    301                                                         350
1   ENAKQFLKEN KDILLMIQEQ IREHYGLDUG GAAPAQEDEA QAQEELEF.S
2   ENAKQFLKEN KDIMLMIQEQ IREHYGLDNN G...VTEKAE EVQEELEFEE
3   ENAKQFLKEN KDIMLMIQEQ IREHYGLDNN G..VVQQQAE ETQEELEFEE
4   ENAKQFLKEN KDIMLMIQEQ IREHYGLDNN G..VVQQQAE ETQEELEFEE
```

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**Figure 2 / Part I**

```
    1                                                                 50
1   ATGAGTGATC GTCAGGCAGC CTTAGATATG GCGCTTAAAC AAATAGAAAA
2   ATGAGTGATC GTCAGGCAGC CTTAGATATG GCTCTTAAGC AAATAGAAAA
3   ATGAGTGATC GTCAGGCAGC CTTAGATATG GCTCTTAAAC AAATAGAAAA
4   ATGAGTGATC GTCAGGCAGC CTTAGATATG GCTCTTAAAC AAATAGAAAA

    51                                                               100
1   GCAGTTTGGT AAAGGTTCGA TTATGAAACT CGGCGAACAA ACTGAAACGA
2   ACAATTCGGC AAAGGTTCCA TCATGAAGCT CGGAGAAAAA ACGGATACAA
3   ACAGTTCGGC AAAGGTTCCA TTATGAAACT GGGAGAAAAG ACAGATACAA
4   ACAGTTCGGC AAAGGTTCCA TTATGAAACT GGGAGAAAAG ACAGATACAA

    101                                                              150
1   GAATTTCAAC AGTTCCGAGC GGTTCTTTAG CGCTCGATGC GGCTCTTGGA
2   GAATTTCAAC GGTGCCGAGC GGTTCCCTTG CACTTGATAC CGCTCTCGGA
3   GAATTTCTAC TGTACCAAGC GGCTCCCTCG CTCTTGATAC AGCACTGGGA
4   GAATTTCTAC TGTACCAAGC GGCTCCCTCG CTCTTGATAC AGCACTGGGA

    151                                                              200
1   GTGGGCGGAT ACCCGCGCGG CCGGATTATT GAAGTATACG GGCCTGAAAG
2   ATAGGCGGAT ACCCGCGCGG ACGGATTATT GAAGTATACG GACCTGAAAG
3   ATTGGCGGAT ATCCTCGCGG ACGGATTATT GAAGTATACG GTCCTGAAAG
4   ATTGGCGGAT ATCCTCGCGG ACGGATTATT GAAGTATACG GTCCTGAAAG

    201                                                              250
1   CTCCGGTAAA ACGACGGTGG CGCTTCATGC GATTGCCGAA GTTCAGCAGC
2   CTCAGGTAAA ACGACTGTAG CGCTTCACGC AATCGCTGAG GTTCAGGAAA
3   CTCAGGTAAA ACAACTGTGG CGCTTCATGC GATTGCTGAA GTTCAGCAGC
4   CTCAGGTAAA ACAACTGTGG CGCTTCATGC GATTGCTGAA GTTCAGCAGC

    251                                                              300
1   AGGGCGGACA AGCGGCGTTC ATCGACGCCG ACACCGCGCT TGATCCCGTC
2   AAGGCGGACA GGCAGCATTT ATTGATGCCG AGCATGCTCT TGATCCTGTG
3   A..GCGGACA AGC.GCGTTT ATCGATGCGG AGCATGCGTT AGATCCGGTA
4   A..GCGGACA AGC.GCGTTT ATCGATGCGG AGCATGCGTT AGATCCGGTA

    301                                                              350
1   TATGCACAAA AGCTGGGCGT CAACATTGAT GAGCTTTTGC TGTCACAGCC
2   TACGCGCAAA AGCTCGGTGT CAATATCGAA GAGCTGCTGC TTTCTCAGCC
3   TACGCGCAAA AGCTCGGTGT TAACATCGAA GAGCTTTTAC TGTCTCAGCC
4   TACGCGCAAA AGCTCGGTGT TAACATCGAA GAGCTTTTAC TGTCTCAGCC
```

**Figure 2 / Part II**

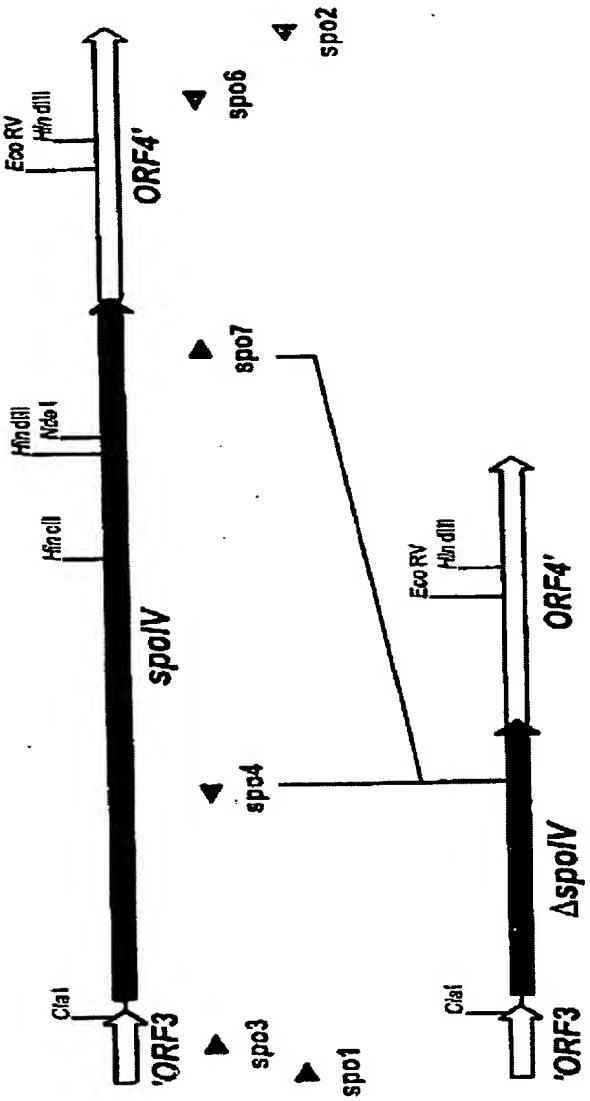
```
    351                                                         400
1   TGATACGGGC GAGCAGGCGC TCGAAATCGC TGAAGCCCTT GTCAGAAGCG
2   GGATACGGGA GAGCAGGCGC TGGAGATTGC TGAAGCGCTG GTGCGAAGCG
3   TGACACAGGC GAGCAGGCGC TTGAAATTGC GGAAGCATTG GTTCGAAGCG
4   TGACACAGGC GAGCAGGCGC TTGAAATTGC GGAAGCATTG GTTCGAAGCG

    401                                                         450
1   GAGCGGTGGA TATCGTTGTC ATCGACTCTG TAGCAGCGCT TGTGCCGAAA
2   GAGCTGTCGA TATCGTAGTC GTTGACTCTG TTGCGGCGCT TGTTCCAAAA
3   GGGCAGTTGA CATTGTCGTT GTCGACTCTG TAGCCGCTCT CGTTCCGAAA
4   GGGCAGTTGA CATTGTCGTT GTCGACTCTG TAGCCGCTCT CGTTCCGAAA

    451                                                         500
1   GCTGAAATCG AAGGAGATAT GGGGGATTCC CACGTCGGTT TGCAGGCCAG
2   GCTGAAATTG AAGGTGACAT GGGTGATTCA CACGTCGGTT TACAGGCGCG
3   GCGGAAATTG AAGGCGACAT GGGAGATTCG CATGTCGGTT TACAAGCACG
4   GCGGAAATTG AAGGCGACAT GGGAGATTCG CATGTCGGTT TACAAGCACG

    501                                                         550
1   ACTGATGTCT CAGGCGCTTC GCAAGCTTTC CGGAGCGATC AATAAATCGA
2   TCTCATGTCT CAGGCGCTCC GTAAGCTTTC CGGCGCCATC AATAAATCTA
3   CTTAATGTCT CAAGCGCTTC GTAAGCTTTC AGGGGCCATT AACAAATCGA
4   CTTAATGTCT CAAGCGCTTC GTAAGCTTTC AGGGGCCATT AACAAATCGA

    551                                                         600
1   AGACCATCGC GATCTTTATC AACCAGATTC GTGAAAAAGT CGGTGTCATG
2   AAACAATCGC AATCTTTATT AACCAGATTC GTGAAAAAGT CGGCGTTATG
3   AGACAATCGC GATTTTCATT AACCAAATTC GTGAAAAAGT CGGTGTTATG
4   AGACAATCGC GATTTTCATT AACCAAATTC GTGAAAAAGT CGGTGTTATG

    601                                                         650
1   TTTGGAAATC CTGAGACGAC GCCAGGCGGA AGAGCGCTGA AATTCTACTC
2   TTCGGAAATC CGGAGACGAC ACCGGGCGGC CGCGCGCTGA AATTCTATTC
3   TTCGGGAACC CGGAAACAAC ACCTGGCGGC CGTGCGTTGA AATTCTATTC
4   TTCGGGAACC CGGAAACAAC ACCTGGCGGC CGTGCGTTGA AATTCTATTC

    651                                                         700
1   TTCTGTCCGC CTTGAAGTGC GCCGCGCAGA GCAGCTGAAA CAAGGCAACG
2   TTCCGTGCGT CTTGAAGTGC GCCGTGCCGA GCAATTAAAG CAGGGCAACG
3   TTCCGTGCGT CTTGAAGTGC GCCGTGCTGA ACAGCTGAAA CAAGGCAACG
4   TTCCGTGCGT CTTGAAGTGC GCCGTGCTGA ACAGCTGAAA CAAGGCAACG
```

**Figure 2 / Part III**

```
    701                                                        750
1   ACGTCATGGG GAACAAGACG AAAATCAAAG TCGTGAAAAA CAAAGTGGCA
2   ACGTTATGGG GAATAAAACG AGAATTAAAG TCGTAAAAAA CAAAGTCGCT
3   ACGTAATGGG GAACAAAACG AAAATCAAAG TCGTGAAAAA CAAGGTGGCT
4   ACGTAATGGG GAACAAAACG AAAATCAAAG TCGTGAAAAA CAAGGTGGCT

    751                                                        800
1   CCTCCATTCC GGACAGCCGA AGTGGACATT ATGTACGGGG AAGGAATTTC
2   CCTCCGTTCC GTACGGCTGA AGTGGACATT ATGTACGGTG AAGGAATCTC
3   CCGCCGTTCC GTACAGCCGA GGTTGACATT ATGTACGGAG AAGGCATTTC
4   CCGCCGTTCC GTACAGCCGA GGTTGACATT ATGTACGGAG AAGGCATTTC

    801                                                        850
1   AAAAGAAGGG GAAATCATCG ACCTCGGAAC AGAGCTTGAC ATCGTTCAAA
2   CAAAGAAGGG GAAATCATCG ACCTTGGAAC TGAACTTGAT ATCGTGCAGA
3   AAAAGAAGGC GAAATCATTG ATCTAGGAAC TGAACTTGAT ATCGTGCAAA
4   AAAAGAAGGC GAAATCATTG ATCTAGGAAC TGAACTTGAT ATCGTGCAAA

    851                                                        900
1   AGAGCGGTGC ATGGTACTCT TATCAGGAGG AACGCCTTGG ACAAGGCCGT
2   AAAGCGGCTC GTGGTATTCT TATGAAGAAG AACGCCTCGG ACAGGGCCGT
3   AAAGCGGTTC ATGGTACTCT TATGAAGAAG AGCGTCTTGG CCAAGGCCGT
4   AAAGCGGTTC ATGGTACTCT TATGAAGAAG AGCGTCTTGG CCAAGGCCGT

    901                                                        950
1   GAAAACGCCA AACAGTTCCT GAAAGAAAAC AAGGATATCC TTTTGATGAT
2   GAAAACGCCA AGCAGTTCTT AAAAGAAAAT AAAGACATCA TGCTGATGAT
3   GAAAATGCAA AACAATTCCT GAAAGAAAAT AAAGATATCA TGCTGATGAT
4   GAAAATGCAA AACAATTCCT GAAAGAAAAT AAAGATATCA TGCTGATGAT

    951                                                       1000
1   TCAAGAGCAG ATCCGGGAGC ACTACGGTTT GGATACTGGA GGCGCTGCTC
2   TCAAGAACAA ATCCGTGAAC ATTACGGTTT GGACAATAAC GGTGTTAC..
3   CCAGGAGCAA ATTCGCGAAC ATTACGGCTT GGATAATAAC GGAGTAGTGC
4   CCAGGAGCAA ATTCGCGAAC ATTACGGCTT GGATAATAAC GGAGTAGTGC

    1001                                                      1050
1   CTGCACAGGA AGACGAGGCC CAAGCTCAGG AAGAACTCGA GTTTTAATCA
2   .......GGA AAAAGCGGAA GAAGTTCAGG AAGAGCTTGA ATTCGAAGAA
3   ......AGCA GCAAGCTGAA GAGACACAAG AAGAACTCGA ATTTGAAGAA
4   ......AGCA GCAAGCTGAA GAGACACAAG AAGAACTCGA ATTTGAAGAA

    1051
1   TGA
2   TAA
3   ...
4   TAA
```

Figure 3

A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spo6
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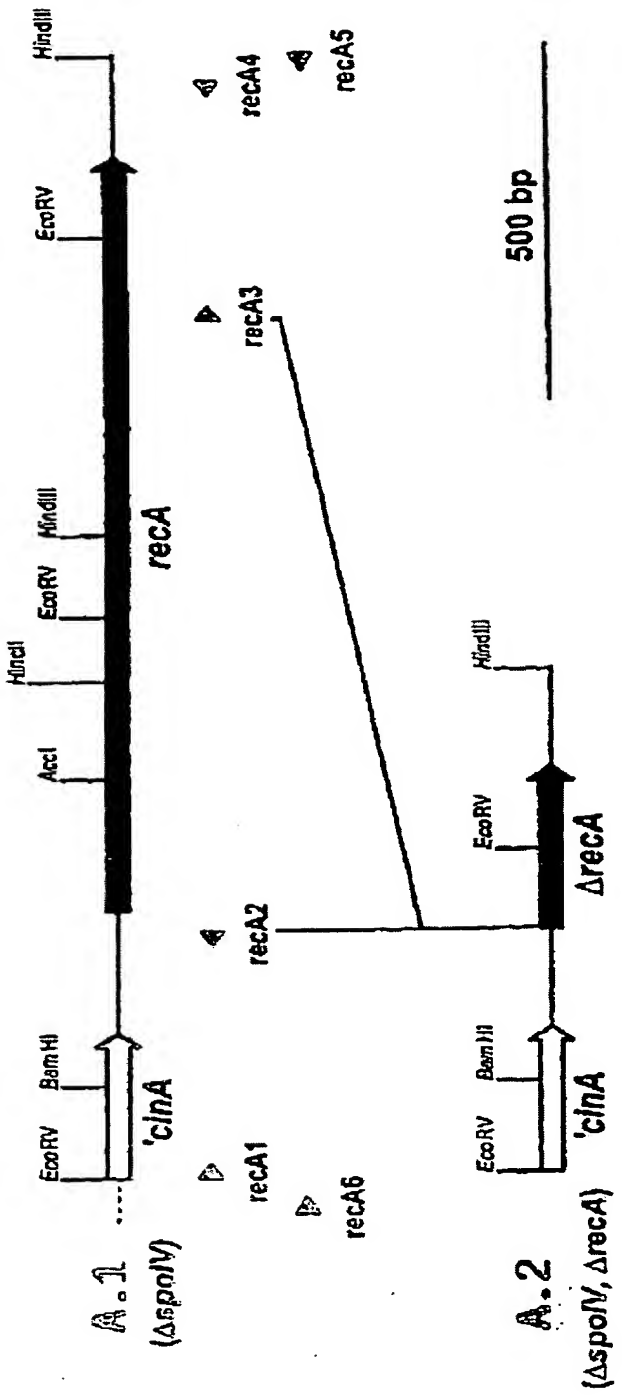
HindIII
ORF4'
spo7
HindIII
NdeI
HincII
spoIV
EcoRV
HindIII
ORF4'
spo4
ΔspoIV
ClaI
'ORF3
ClaI
'ORF3
spo3
spo1

A.1

Figure 3

B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EcoRV
HindIII
EcoRV
NheI
AccI
recA
EcoRV
BamHI
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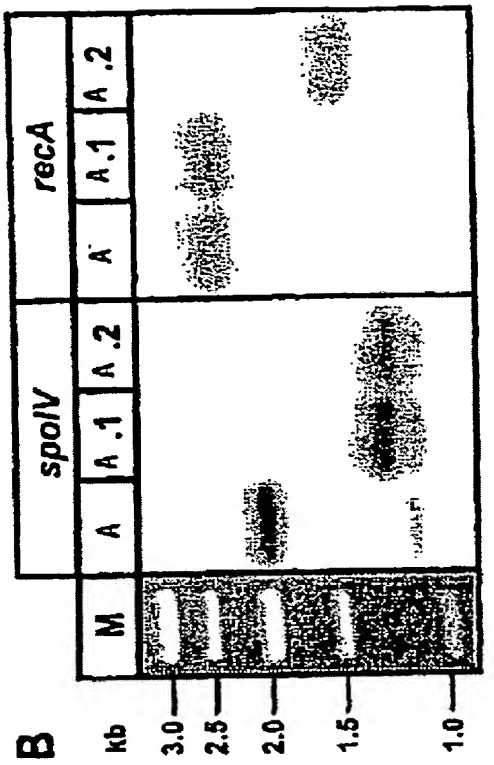
A.1
(ΔspoIV)
recA1
recA6
recA4
recA5
recA3
recA2
500 bp
HindIII
EcoRV
ΔrecA
EcoRV
BamHI
'clnA
A.2
(ΔspoIV, ΔrecA)

Figure 4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kb
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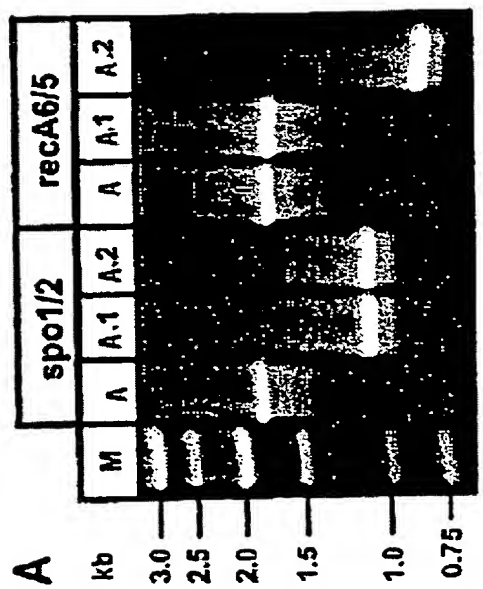
M
spoIV
A
A.1
A.2
recA
A
A.1
A.2


A
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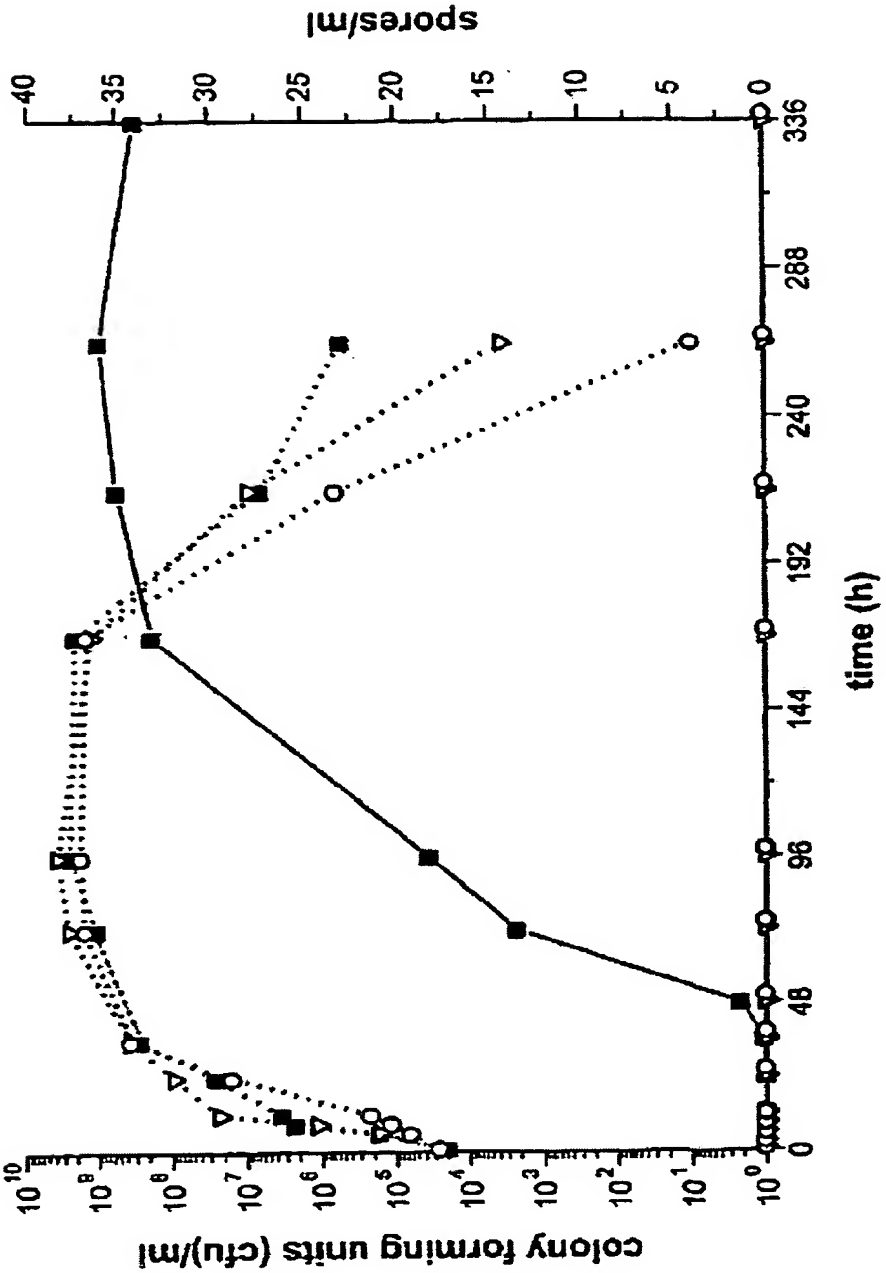
A.2
recA6/5
A
A.1
A.2

Figure 5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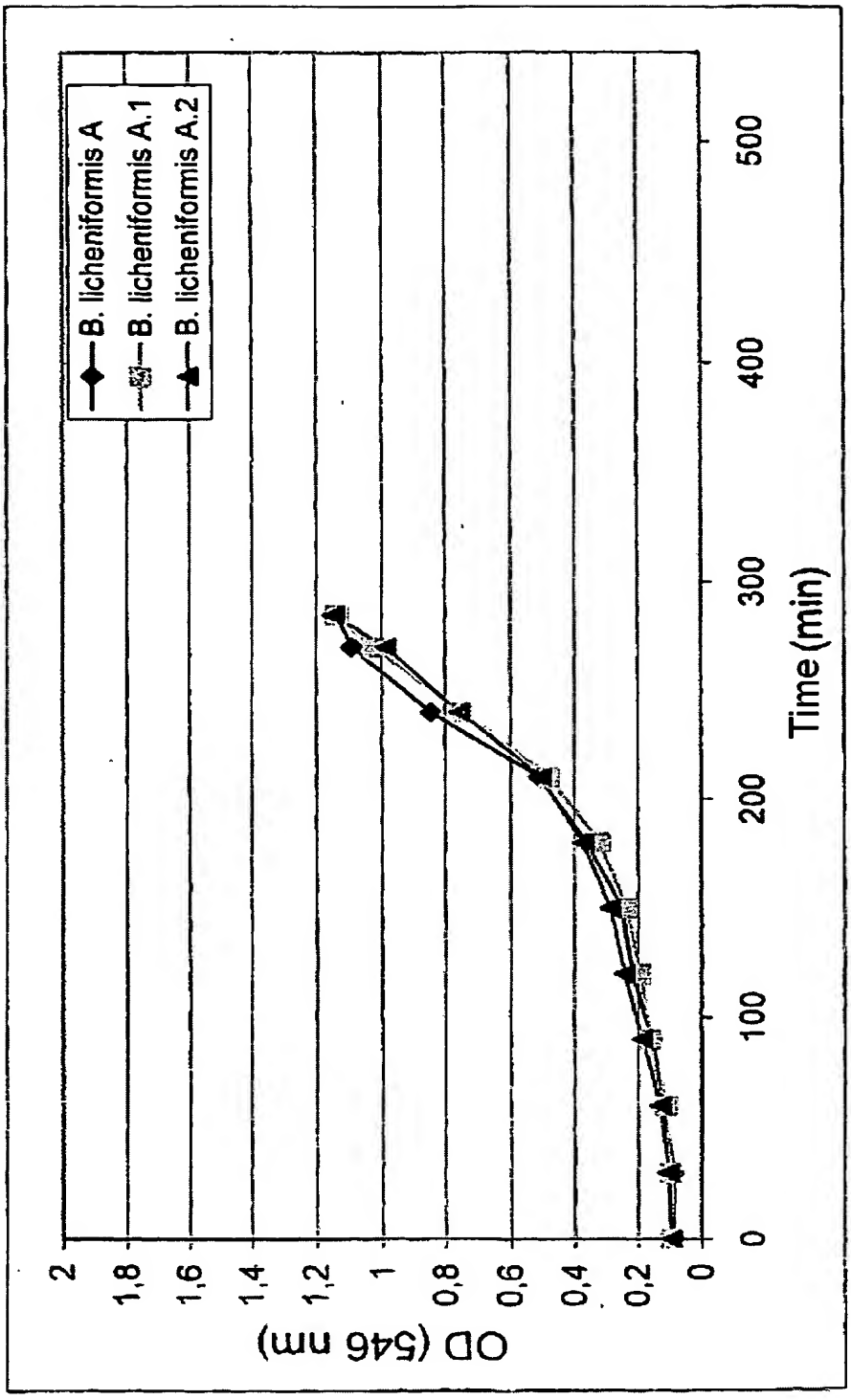
35
30
25
20
15
10
5
0
336
288
240
192
144
96
48
0
time (h)
colony forming units (cfu)/ml
$10^{10}$
$10^{9}$
$10^{8}$
$10^{7}$
$10^{6}$
$10^{5}$
$10^{4}$
$10^{3}$
$10^{2}$
$10^{1}$
$10^{0}$

**Figure 6**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B. licheniformis A.2
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0
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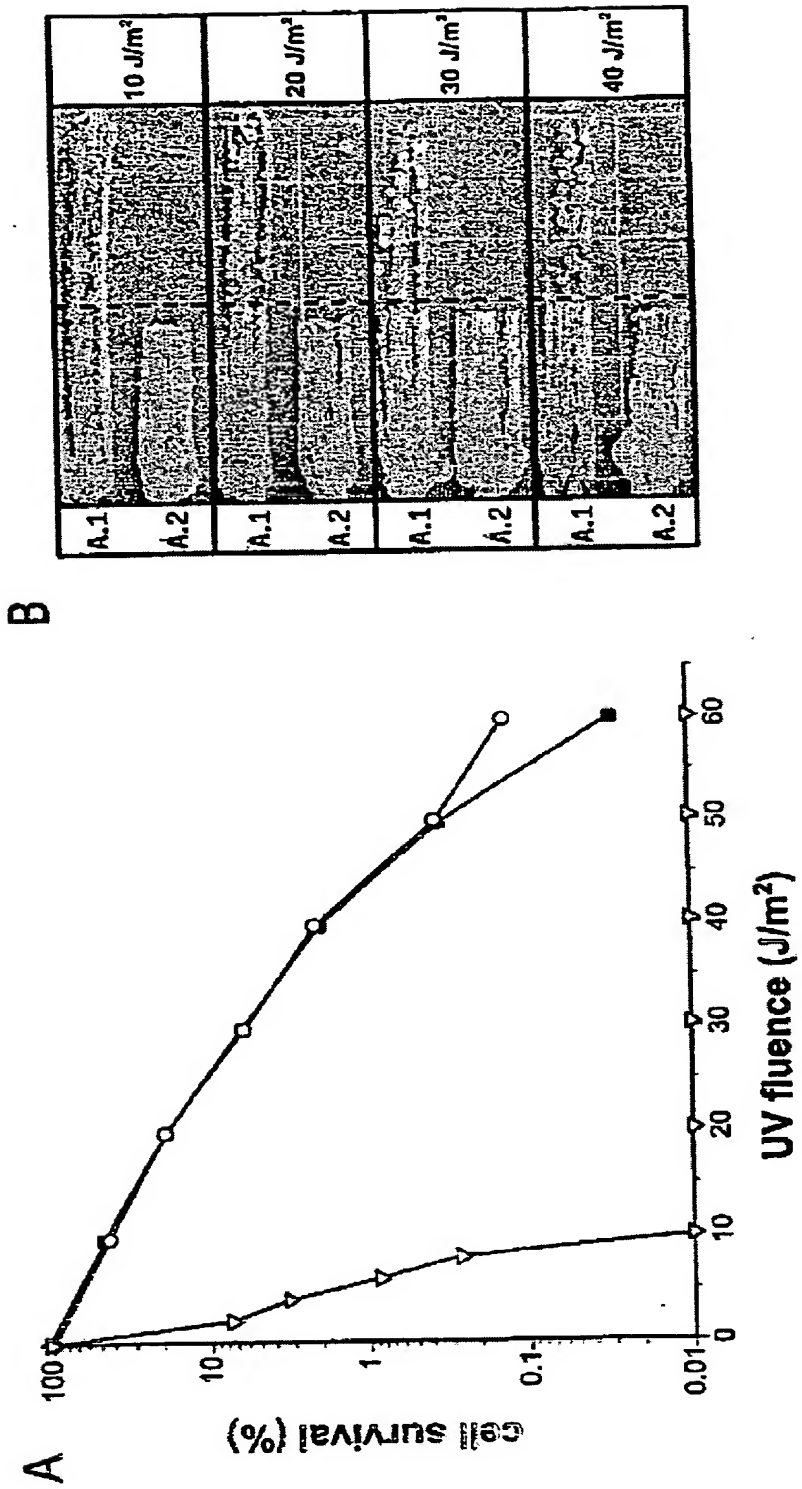
200
300
400
500

Figure 7


B
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20 J/m²
30 J/m²
40 J/m²
A.1
A.2
A
Cell survival (%)
100
10
1
0.1
0.01
0
10
20
30
40
50
60
UV fluence (J/m²)

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